



## SEQUENCE LISTING

<110> Waldman, Scott A.  
Pearlman, Joshua M.  
Barber, Michael T.  
Schulz, Stephanie  
Parkinson, Scott J.

<120> Compositions that Specifically Bind to Colorectal Cancer Cells and Methods of Using the Same

<130> 08321-0152 CT1 (TJU0007-103)

<140> 10/656,895  
<141> 2003-09-05

<150> US 09/649,697  
<151> 2000-08-28

<150> US 08/908,643  
<151> 1997-08-07

<160> 82

<170> PatentIn version 3.3

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Pro Gly Trp Leu Ser Phe Ser Ser Gln Ala  
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ccagctgaga agttgatata cttcttggtt aactttgga aaacccaacga tctgccctc  
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Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala Gln Arg  
20 25 30

Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser Thr Phe Gln  
35 40 45

Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala Gly Ser  
50 55 60

Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu Met Ser  
65 70 75 80

Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp Lys Thr Asn  
85 90 95

Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val Tyr Lys  
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gaaaccttaa ccaggctgat gtctccagct agaaagttga tatacttctt ggtaacttt  
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tggaaaacca acgatctgcc cttcaaaact tattcctgga gcacttcgta tgtttacaag  
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Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala Gly Ser  
20 25 30

Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu Met Ser  
35 40 45

Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp Lys Thr Asn  
50 55 60

Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val Tyr Lys  
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ttgggtaact tttggaaaac caacgatctg cccttcaaaa cttattcctg gagcacttcg  
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<400> 9

Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile Ser Ala Gly Ser  
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Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu Thr Arg Leu Met Ser  
20 25 30

Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp Lys Thr Asn  
35 40 45

Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val Tyr Lys  
50 55 60

Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val Pro  
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cccttcaaaa cttattcctg gagcacttcg tatgtttaca agaatggtag agaaaactgag  
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<400> 11

Met Ile Ser Ala Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr  
1 5 10 15

Leu Thr Arg Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val  
20 25 30

Asn Phe Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser  
35 40 45

Thr Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu  
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120

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<210> 13  
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<400> 13

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Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser Tyr Val  
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Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val Pro  
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<210> 14

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Met His Asn Gly Trp Ala Val Ser Ser  
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<400> 17

Met Tyr Ile Leu His Leu Pro Asp Val Pro  
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Met Phe Thr Arg Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr Leu  
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Asn Ala Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe  
20 25 30

Lys Val Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp  
35 40 45

His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe  
50 55 60

Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val Ile  
65 70 75 80

Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr  
85 90 95

Ala Pro Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly  
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Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val Val Leu

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25

30

Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His Asn Arg Lys  
35 40 45

Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe Leu Tyr Lys Leu  
50 55 60

Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val Ile Ile Leu Val Asp  
65 70 75 80

Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr  
85 90 95

Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser  
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Lys

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Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile  
20 25 30

Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn  
35 40 45

Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu Ser  
50 55 60

Pro Gly Glu Phe Pro Ser Lys  
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Val Ala Glu Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln  
20 25 30

Tyr Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu  
35 40 45

Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys  
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<210> 26  
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<210> 27

<211> 17  
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<400> 27

Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser  
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Lys

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<211> 57  
<212> DNA  
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<400> 28

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Arg Trp Cys

<210> 30  
<211> 42  
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<210> 33  
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<400> 33

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<210> 34  
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<400> 34  
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<210> 35  
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<400> 35

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<210> 36  
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<400> 36

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<400> 37

Met Leu Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro Lys  
1 5 10 15

Phe Ala His Ala Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp Gly Pro  
20 25 30

Val Thr Leu Gly  
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<212> DNA  
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<210> 39

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<400> 39

Met Glu Lys Ile Leu Pro Pro Pro Asn Leu Leu Met Leu Ser Gly Ile  
1 5 10 15

Ser Leu Leu Lys Gly Met Thr Val Gln  
20 25

<210> 40  
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<212> PRT  
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<400> 41

Met Leu Ser Gly Ile Ser Leu Leu Lys Gly Met Thr Val Gln  
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<210> 42  
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<212> DNA  
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gaaatacaag gttctttgga ccta  
84

<210> 43  
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Met Thr Gly Gly Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr Leu  
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Cys Gly His Gln Glu Ile Gln Gly Ser Leu Asp Leu  
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<210> 44  
<211> 72  
<212> DNA  
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tctttggacc ta  
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<212> PRT  
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<400> 45

Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr Leu Cys Gly His Gln  
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Glu Ile Gln Gly Ser Leu Asp Leu  
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<210> 46  
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<220>  
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<400> 47

Met Val Leu Pro Leu Tyr Pro Leu Trp Thr Pro Arg Asn Thr Arg Phe  
1 5 10 15

Phe Gly Pro Met Ile Pro Thr Leu Ile Arg Thr Ile Leu Trp Ile  
20 25 30

<210> 48  
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<212> DNA  
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<400> 48  
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<210> 49  
<211> 12  
<212> PRT  
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<400> 49

Met Ile Pro Thr Leu Ile Arg Thr Ile Leu Trp Ile  
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<210> 50  
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<212> DNA  
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<220>  
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gtcgctctcc tgatgcttag aaaaatataga aaagattatg aacttcgtca gaaaaaaatgg  
180

tcccacattc ctcctgaaaa tatcttcctt ctggagacca atgagaccaa tcatagttagc  
240

ctcaagatcg atgatgacaa aagacgagat acaatccaga gactacgaca gtgcaaatac  
300

gacaaaaagc gagtgattct caaagatctc aagcacaatg atggtaattt cactgaaaaa  
360

cagaagatag aattgaacaa gttgcttcag aaagactatt acaacctgac caagttctac  
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ggcacagtga aacttgatac catgatcttc ggggtgatag aatactgtga gagaggatcc  
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cctccgggaa gttttaaa  
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<210> 51  
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<223> Synthetic Construct

<400> 51

Met Ser Pro Thr Phe Thr Trp Lys Asn Ser Lys Leu Pro Asn Asp Ile  
1 5 10 15

Thr Gly Arg Gly Pro Gln Ile Leu Met Ile Ala Val Phe Thr Leu Thr  
20 25 30

Gly Ala Val Val Leu Leu Leu Val Ala Leu Leu Met Leu Arg Lys  
35 40 45

Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp Ser His Ile Pro  
50 55 60

Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu Thr Asn His Val Ser  
65 70 75 80

Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg Leu Arg  
85 90 95

Gln Cys Lys Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu Lys His  
100 105 110

Asn Asp Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn Lys Leu  
115 120 125

Leu Gln Lys Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr Val Lys  
130 135 140

Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser  
145 150 155 160

Pro Pro Gly Ser Phe Lys  
165

<210> 52

<211> 426

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 52

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60

atgctcagaa aatataaaaa agattatgaa ctgcgtcaga aaaaatggtc ccacattcct  
120

cctgaaaata tctttcctct ggagaccaat gagaccaatc atgttagcct caagatcgat  
180

gatgacaaaa gacgagatac aatccagaga ctacgacagt gcaaatacga caaaaagcga  
240

gtgattctca aagatctcaa gcacaatgtat ggtaatttca ctgaaaaaca gaagatagaa  
300

ttgaacaagt tgcttcagaa agactattac aacctgacca agttctacgg cacagtgaaa  
360

cttgataccca tgatcttcgg ggtgatagaa tactgtgaga gaggatcccc tccggaaagt  
420

tttaaa  
426

<210> 53  
<211> 142  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 53

Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu Leu  
1 5 10 15

Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg  
20 25 30

Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu  
35 40 45

Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg  
50 55 60

Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg  
65                   70                   75                   80

Val Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys  
85                   90                   95

Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr Asn Leu  
100               105               110

Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe Gly Val  
115               120               125

Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly Ser Phe Lys  
130               135               140

<210> 54

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 54

atgctcagaa aatatagaaa agattatgaa cttcgtaaga aaaaatggtc ccacattcct  
60

cctgaaaata tctttcctct ggagaccaat gagaccaatc atgttagcct caagatcgat  
120

gatgacaataa gacgagatac aatccagaga ctacgacagt gcaaatacga caaaaagcga  
180

gtgattctca aagatctcaa gcacaatgtat ggtaatttca ctgaaaaaca gaagatagaa  
240

ttgaacaagt tgcttcagaa agactattac aacctgacca agttctacgg cacagtgaaa  
300

cttgatacca tgatcttcgg ggtgatagaa tactgtgaga gaggatcccc tccgggaagt  
360

ttaaaa  
366

<210> 55  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 55

Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp  
1 5 10 15

Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu Thr  
20 25 30

Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp Thr Ile  
35 40 45

Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val Ile Leu Lys  
50 55 60

Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu  
65 70 75 80

Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr  
85 90 95

Gly Thr Val Lys Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys  
100 105 110

Glu Arg Gly Ser Pro Pro Gly Ser Phe Lys

115

120

<210> 56  
<211> 57  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Construct  
  
<400> 56  
atgatcttcg gggtgataga atactgtgag agaggatccc ctccgggaag ttttaaa  
57

<210> 57  
<211> 19  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Construct  
  
<400> 57  
  
Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly  
1 5 10 15

Ser Phe Lys

<210> 58  
<211> 30  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Construct  
  
<400> 58  
atgatattac aggccggggc cctcagatcc  
30

<210> 59  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 59

Met Ile Leu Gln Ala Gly Ala Leu Arg Ser  
1 5 10

<210> 60  
<211> 156  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 60  
atgaacttcg tcagaaaaaa tggtcccaca ttcctcctga aaatatcttt cctctggaga  
60

ccaatgagac caatcatgtt agcctaaga tcgatgatga caaaagacga gatacaatcc  
120

agagactacg acagtgcaaa tacgacaaaaa agcgag  
156

<210> 61  
<211> 52  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 61

Met Asn Phe Val Arg Lys Asn Gly Pro Thr Phe Leu Leu Lys Ile Ser  
1 5 10 15

Phe Leu Trp Arg Pro Met Arg Pro Ile Met Leu Ala Ser Arg Ser Met  
20 25 30

Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr  
35 40 45

Thr Lys Ser Glu  
50

<210> 62  
<211> 93  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 62  
atgagaccaa tcatgttagc ctcaagatcg atgatgacaa aagacgagat acaatccaga  
60

gactacgaca gtgcaaatac gacaaaaagc gag  
93

<210> 63  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 63

Met Arg Pro Ile Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp Glu  
1 5 10 15

Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser Glu  
20 25 30

<210> 64  
<211> 81  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 64  
atgttagctt caagatcgat gatgacaaaa gacgagatac aatccagaga ctacgacagt  
60  
  
gcaaatacga caaaaagcga g  
81

<210> 65  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 65  
  
Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp Glu Ile Gln Ser Arg  
1 5 10 15

Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser Glu  
20 25

<210> 66  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 66  
atgatgacaa aagacgagat acaatccaga gactacgaca gtgcaaatac gacaaaaagc

60

gag  
63

<210> 67  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 67

Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn  
1                       5                                   10                           15

Thr Thr Lys Ser Glu  
20

<210> 68  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 68  
atgacaaaag acgagataca atccagagac tacgacagtg caaatacgac aaaaagcggag  
60

<210> 69  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 69

Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr  
1                   5                   10                   15

Thr Lys Ser Glu  
20

<210> 70  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 70  
atggtcccac attcctcc  
18

<210> 71  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 71

Met Val Pro His Ser Ser  
1                   5

<210> 72  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 72  
atgatggtaa tttcactgaa aaacagaaga

30

<210> 73  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 73

Met Met Val Ile Ser Leu Lys Asn Arg Arg  
1 5 10

<210> 74  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 74  
atggtaattt cactgaaaaa cagaaga  
27

<210> 75  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 75

Met Val Ile Ser Leu Lys Asn Arg Arg  
1 5

<210> 76  
<211> 42

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Construct  
  
<400> 76  
atggcgccg ggagcatgcg acgtcggccc attcgcccta ta  
42

<210> 77  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct  
  
<400> 77

Met Ala Ala Gly Ser Met Arg Arg Arg Pro Ile Arg Pro Ile  
1                       5                                   10

<210> 78  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct  
  
<400> 78  
atgcgacgtc ggcccatcg ccctata  
27

<210> 79  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 79

Met Arg Arg Arg Pro Ile Arg Pro Ile  
1 5

<210> 80  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 80  
atgacacaat ttcct  
15

<210> 81  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Construct

<400> 81

Met Thr Gln Phe Pro  
1 5

<210> 82  
<211> 3787  
<212> DNA  
<213> Homo sapiens

<400> 82  
tggagtgggc tgagggactc cactagaggc tgtccatctg gattccctgc ctcccttagga  
60

gcccaacaga gcaaagcaag tgggcacaag gagtatggtt ctaacgtgat tgggtcatg  
120

aagacgttgc tggactt ggctttgtgg tcactgctct tccagcccg gtggctgtcc

180

ttagttccc aggtgagtca gaactgccac aatggcagct atgaaatcag cgtcctgatg  
240

atgggcaact cagcccttgc agagcccctg aaaaacttgg aagatgcggt gaatgagggg  
300

ctggaaatag tgagaggacg tctgcaaaat gctggcctaa atgtgactgt gaacgctact  
360

ttcatgtatt cgatggtct gattcataac tcaggcgact gccggagtag cacctgtgaa  
420

ggcctcgacc tactcaggaa aatttcaaat gcacaacgga tgggctgtgt cctcataggg  
480

ccctcatgta catactccac cttccagatg taccttgaca cagaatttag ctaccccatg  
540

atctcagctg gaagttttgg attgtcatgt gactataaag aaaccttaac caggctgatg  
600

tctccagcta gaaagttgat gtacttcttg gttaactttt ggaaaaccaa cgatctgccc  
660

ttcaaaactt attcctggag cacttcgtat gtttacaaga atggcacaga aactgaggac  
720

tgttctggc accttaatgc tctggaggct agcgttcct atttctccca cgaactcggc  
780

tttaaggtgg tgttaagaca agataaggag tttcaggata tcttaatgga ccacaacagg  
840

aaaagcaatg tgattattat gtgtggtggt ccagagttcc tctacaagct gaagggtgac  
900

cgagcagtgg ctgaagacat tgtcattatt ctatggatc tttcaatga ccagtacttg  
960

gaggacaatg tcacagcccc tgactatatg aaaaatgtcc ttgttctgac gctgtctcct  
1020

ggaaattccc ttctaaatag ctcttctcc aggaatctat caccaacaaa acgagacttt  
1080

cgcttcgcct atttgaatgg aatcctcgac tttggacata tgctgaagat atttcttcaa  
1140

aatggagaaa atattaccac ccccaaattt gctcatgcct tcaggaatct cactttgaa  
1200

gggtatgacg gtccagtgac cttggatgac tggggggatg ttgacagtagc catggtgctt  
1260

ctgtatacct ctgtggacac caagaaatac aaggttctt tgacctatga tacccacgta  
1320

aataagacct atcctgtgga tatgagcccc acattcactt ggaagaactc taaacttcct  
1380

aatgatatta caggccgggg ccctcagatc ctgatgattt cagtctcac cctcaactgga  
1440

gctgtggtgc tgctcctgct cgtcgtctc ctgatgctca gaaaatatacg aaaagattat  
1500

gaacttcgtc agaaaaatg gtcccacatt cctcctgaaa atatcttcc tctggagacc  
1560

aatgagacca atcatgttag cctcaagatc gatgatgaca aaagacgaga tacaatccag  
1620

agactacgac agtcaaata cgtcaaaaag cgagtgattt tcaaagatct caagcacaat  
1680

gatggtaatt tcactgaaaa acagaagata gaattgaaca agttgcttca gattgactat  
1740

tacaccctaa ccaagttcta cgggacagtg aaactggata ccatgatctt cgggggtgata  
1800

gaatactgtg agagaggatc cctccgggaa gtttaaatg acacaatttc ctaccctgat  
1860

ggcacattca tggattggga gtttaagatc tctgtcttgt atgacattgc taaggaaatg  
1920

tcatatctgc actccagtaa gacagaagtc catggtcgtc tgaaatctac caactgcgtt  
1980

gtggacagta gaatggtggt gaagatcaact gattttggct gcaattccat tttgcctcca  
2040

aaaaaggacc tgtggacagc tccagagcac ctccgccaag ccaacatctc tcagaaagga  
2100

gatgtgtaca gctatggat catcgacacag gagatcattc tgcggaaaga aaccttctac  
2160

actttgagct gtcgggaccg gaatgagaag attttcagag tggaaaattc caatggaatg  
2220

aaacccttcc gcccagattt attcttggaa acagcagagg aaaaagagct agaagtgtac  
2280

ctacttgtaa aaaactgttg ggaggaagat ccagaaaaga gaccagattt caaaaaaatt  
2340

gagactacac ttgccaagat atttggactt tttcatgacc aaaaaaatga aagctataatg  
2400

gataccttga tccgacgtct acagctatat tctcgaaacc tggaacatct gtagaggaa  
2460

aggacacagc tgtacaaggc agagagggac agggctgaca gacttaactt tatgttgctt  
2520

ccaaggctag tggtaaagtc tctgaaggag aaaggcttg tggagccgga actatatgag  
2580

gaagttacaa tctacttcag tgacattgta gtttcacta ctatctgcaa atacagcacc  
2640

cccatggaag tggtgacat gcttaatgac atctataaga gtttgacca cattgttgat  
2700

catcatgatg tctacaaggt ggaaaccatc ggtgatgcgt acatggtggc tagtggttg  
2760

cctaagagaa atggcaatcg gcatgcaata gacattgcca agatggcctt gggaaatcctc  
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agcttcatgg ggaccttga gctggagcat cttcctggcc tcccaatatg gattcgcatt  
2880

ggagttcaact ctggccctg tgctgctgga gttgtggaa tcaagatgcc tcgttattgt

2940

ctatggag atacggtcaa cacagcctct agatggaaat ccactggcct cccttgaga  
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attcacgtga gtggctccac catagccatc ctgaagagaa ctgagtgcca gttcctttat  
3060

gaagtgagag gagaaacata cttaaaggaa agagggaaatg agactaccta ctggctgact  
3120

gggatgaagg accagaaatt caacctgcca acccctccta ctgtggagaa tcaacagcgt  
3180

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3240

ataagaagcc aaaaacccag acggtagcc agctataaaa aaggcactct ggaataacttg  
3300

cagctgaata ccacagacaa ggagagcacc tattttaaa cctaaatgag gtataaggac  
3360

tcacacaaat taaaatacag ctgcactgag gccaggcacc ctcaggtgtc ctgaaagcct  
3420

acttcctga gacctcatga ggcagaaatg tcttaggctt ggctgccctg tttggaccat  
3480

ggactttctt tgcatgaatc agatgtgttc tcagtgaaat aactaccttc cactctggaa  
3540

ccttattcca gcagttgttc cagggagctt ctacctggaa aagaaaagaa tttcatttat  
3600

ttttgtttg tttatttta tcgttttgt ttactggctt tccttctgtt ttcataagat  
3660

ttttaaatt gtcataatta tattttaaat acccatcttc attaaagtat atttaactca  
3720

taattttgc agaaaatatg ctatataatta ggcaagaata aaagctaaag gtttcccaa  
3780

aaaaaaa  
3787